Remarks

Paper and computer readable forms of a substitute sequence listing accompany this amendment. I believe the contents of the computer readable form and the paper copy of the substitute sequence listing are identical. The substitute sequence listing contains only those sequences present in the application and in the original sequence listing as filed. Because the computer readable form of the sequence listing was made with a different computer program, however, a paper copy is provided for consistency.

The specification and elected claims have been amended to insert sequence identifiers. The amendments add no new matter.

Please continue to address all correspondence in this application to Joseph H. Guth, Chiron Corporation, Intellectual Property – R440, P.O. Box 8097, Emeryville, CA 94662-8097, telephone (510)-923-3888, fax (510)-655-3542.

Respectfully submitted,

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Appendix 1. Version of the amended paragraphs and claims, with markings to show changes made

22. (amended) A composition consisting essentially of a polynucleotide having a sequence encoding a human fibroblast growth factor receptor (hFGFr) comprising three immunoglobulinlike domains, wherein the sequence is selected from the group consisting of:

(a) the sequence of a cDNA molecule or complement obtainable as follows:

providing oligonucleotide probes

ATAACGGACCTTGTAGCCTCCAATTCTGTG (SEQ ID NO:7) and

GCGGCGTTTGAGTCCGCCATTGGCAAGCTG (SEQ ID NO:8),

providing a cDNA library of candidates,

contacting the cDNA library with the probes under conditions that permit hybridization, and

identifying and isolating the candidate that hybridizes to both oligonucleotides probes;

(b) the sequence encoding SEQ ID NO: 1;

(c) a sequence encoding hFGFr having a sequence substantially the same as the sequence of (a), wherein the differences between the sequences of (c) and (a) are confined to changes in nucleotide sequence which do not result in a change in the corresponding encoded amino acid of hFGFr.

23. (amended) The composition of claim 22, wherein the polynucleotide has a sequence of a cDNA molecule or complement obtainable as follows:

providing oligonucleotide probes

ATAACGGACCTTGTAGCCTCCAATTCTGTG (SEQ ID NO:7) and

GCGGCGTTTGAGTCCGCCATTGGCAAGCTG (SEQ ID NO:8);

providing a cDNA library of candidates;

contacting the cDNA library with the probes under conditions that permit hybridization; and

identifying and isolating the candidate that hybridizes to both oligonucleotide probes.

32. (amended) The composition of claim 31, wherein the nucleic acid encoding means is a polynucleotide having a sequence selected from the group consisting of:

(a) a cDNA molecule or complement obtainable as follows:

providing oligonucleotide probes

ATAACGGACCTTGTAGCCTCCAATTCTGTG (SEQ ID NO:7) and

GCGGCGTTTGAGTCCGCCATTGGCAAGCTG (SEQ ID NO:8),

providing a cDNA library of candidates,

contacting the cDNA library with the probes under conditions that permit hybridization, and

identifying and isolating the candidate that hybridizes to both oligonucleotide probes;

(b) a sequence that encodes SEQ ID NO: 1.

(c) a sequence encoding hFGFr having a sequence substantially the same as the sequence of (a), wherein the differences between said sequence and the sequence of (a) are confined to changes in nucleotide sequence which do not result in a change in the corresponding encoded amino acid of hFGFr.

37. (amended) A method of isolating a polynucleotide having a sequence encoding a human fibroblast growth factor receptor (hFGFr) comprising three

immunoglobulinlike domains, wherein the method comprises:

providing oligonucleotide probes

ATAACGGACCTTGTAGCCTCCAATTCTGTG (SEQ ID NO:7) and

GCGGCGTTTGAGTCCGCCATTGGCAAGCTG (SEQ ID NO:8),

providing a cDNA library of candidates,

contacting the cDNA library with the probes under conditions that permit hybridization, and

identifying and isolating the candidate that hybridizes to both oligonucleotide probes.

41. (amended) The host cell of claim 40, wherein the nucleic acid encoding means is a polynucleotide having a sequence selected from the group consisting of:

(a) the sequence of a cDNA molecule or complement obtainable as follows:

providing oligonucleotide probes

ATAACGGACCTTGTAGCCTCCAATTCTGTG (SEQ ID NO:7) and

GCGGCGTTTGAGTCCGCCATTGGCAAGCTG (SEQ ID NO:8),

providing a cDNA library of candidates,

contacting the cDNA library with the probes under conditions that permit hybridization, and

identifying and isolating the candidate that hybridizes to both oligonucleotide probes;

(b) the sequence encoding SEQ ID NO: 1; and

(c) a sequence encoding hFGFr having a sequence substantially the same as the sequence of (a), wherein the differences between the sequences of (c) and (a) are confined to changes in nucleotide sequence which do not result in a change in the corresponding encoded

amino acid of hFGFr.

43. (amended) The host cell of claim 42, wherein the nucleic acid encoding means is a polynucleotide having the sequence selected from the group consisting of

(a) a cDNA molecule or complement obtainable as follows:

providing oligonucleotide probes

ATAACGGACCTTGTAGCCTCCAATTCTGTG (SEQ ID NO:7) and

GCGGCGTTTGAGTCCGCCATTGGCAAGCTG (SEQ ID NO:8),

providing a cDNA library of candidates,

contacting the cDNA library with the probes under conditions that permit hybridization, and

identifying and isolating the candidate that hybridizes to both oligonucleotide probes;

(b) a sequence that encodes SEQ ID NO: 1; and

(c) a sequence encoding hFGFr having a sequence substantially the same as the sequence of (a), wherein the differences between said sequence and the sequence of (a) are confined to changes in nucleotide sequence which do not result in a change in the corresponding encoded amino acid of hFGFr.

45. (amended) The method of claim 44, wherein the nucleic acid encoding means is a polynucleotide having a sequence selected from the group consisting of:

(a) the sequence of a cDNA molecule or complement obtainable as follows:

providing oligonucleotide probes

ATAACGGACCTTGTAGCCTCCAATTCTGTG (SEQ ID NO:7) and

GCGGCGTTTGAGTCCGCCATTGGCAAGCTG (SEQ ID NO:8),

providing a cDNA library of candidates,

contacting the cDNA library with the probes under conditions that permit hybridization, and

identifying and isolating the candidate that hybridizes to both oligonucleotide probes;

(b) the sequence encoding SEQ ID NO: 1; and

(c) a sequence encoding hFGFr having a sequence substantially the same as the sequence of (a), wherein the differences between the sequences of (c) and (a) are confined to changes in nucleotide sequence which do not result in a change in the corresponding encoded amino acid of hFGFr.

47. (amended) The method of claim 46, wherein the nucleic acid encoding means is a polynucleotide having a sequence selected from the group consisting of:

(a) a cDNA molecule or complement obtainable as follows:

providing oligonucleotide probes

ATAACGGACCTTGTAGCCTCCAATTCTGTG (SEQ ID NO:7) and

GCGGCGTTTGAGTCCGCCATTGGCAAGCTG (SEQ ID NO:8),

providing a cDNA library of candidates,

contacting the cDNA library with the probes under conditions that permit hybridization, and

identifying and isolating the candidate that hybridizes to both oligonucleotide probes;

(b) a sequence that encodes SEQ ID NO: 1; and

(c) a sequence encoding hFGFr having a sequence substantially the same as the sequence of (a), wherein the differences between said sequence and the sequence of (a) are confined to change in nucleotide sequence which do not result in a change in the corresponding

encoded amino acid of hFGFr.

(1) On page 6, line 16:

Figure 2 depicts an amino acid sequence comparison of the six different human FGF receptor forms. Sequences have been aligned for maximum identity and those that differ or are deleted have been boxed. Various domains (abbreviations as in Fig. 1) and regions used for PCR primers (P1-P4) are indicated above sequence 1 (*flg* 5, SEQ ID NO:1). The putative signal peptidase cleavage site is also indicated (↓). Sequence 2 (SEQ ID NO:2) was from A. Isacchi *et al., supra* and sequences 3-6 (SEQ ID NOS:3-6) were from D.E. Johnson *et al., supra.*

(2) On page 14, line 11:

Oligonucleotide adapters, probes and sequencing primers were synthesized by the phosphoramidite method using Applied Biosystems (Foster City, Calif.) model 380A and 380B synthesizers, purified by polyacrylamide gel electrophoresis and desalted on SEP-PAK C_{18} cartridges (Waters, Milford, Mass.). The oligonucleotide probes used for screening the cDNA library were complementary to nucleotides 1-30 (5'-A-TAACGGACCTTGTAGCCTCCAATTCTGTG-3', SEQ ID NO:7) and nucleotides 1840-1869 (5'-GCGGCGTTTGAGTCCGCCATTGGCAAGCTG-3', SEQ ID NO:8) of the published *flg* nucleic acid sequence (M. Ruta *et al., supra*). The two PCR primers used to amplify the extracellular region of the FGF receptor (*flg*5) cDNA consisted of a sense primer, P4 (5'-CCAACCTCTAGAGGATCCACTGGGATGTGGAGCTGGAAGTGC-3', SEQ ID NO:9) containing the ribosome binding site plus amino acids 1-6 of FIG. 5 and an antisense primer, P3 (5'-GTAAGCGGCCGCGGATCCTTACTACTCCAGGTACAGGGGCGA-3', SEQ ID NO:10)

containing amino acids 369-374 of *flg*5 and directly followed by a termination codon. Both primers contain BamHI sites to facilitate cloning into pAc373. Two additional PCR primers were used to identify two and three immunoglobulinlike domain FGF receptors in various tissues. They were a sense primer, P1 (5'-CCATTTGGATCCGTCACAGCCACACTCTGCACCGCT-3', SEQ ID NO:11) encoding amino acids 14 to 21 of *flg* 5 and an antisense primer P2 (5'-CCATTTGTCGACTTCCATCTTTTCTGGGGATGTCCA-3', SEQ ID NO:12) encoding the complement of amino acids 154 to 161 of *flg* 5. The primers contain BamHI and SalI sites to facilitate cloning into M13 sequencing plasmids.